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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/545,998

DATE: 07/28/2004

TIME: 14:14:16

Input Set : N:\CrF3\RULE60\09545998.raw
 Output Set: N:\CRF4\07282004\I545998.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Gorman, Daniel M.
 6 Randall, Troy D.
 7 Zlotnik, Albert

9 (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED
 10 REAGENTS

12 (iii) NUMBER OF SEQUENCES: 8
 14 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: DNAX Research Institute
 16 (B) STREET: 901 California Avenue
 17 (C) CITY: Palo Alto
 18 (D) STATE: California
 19 (E) COUNTRY: USA
 20 (F) ZIP: 94304-1104

22 (v) COMPUTER READABLE FORM:

23 (A) MEDIUM TYPE: Floppy disk
 24 (B) COMPUTER: IBM PC compatible
 25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 26 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

28 (vi) CURRENT APPLICATION DATA:

C--> 29 (A) APPLICATION NUMBER: US/09/545,998
 C--> 30 (B) FILING DATE: 10-Apr-2000
 W--> 35 (C) CLASSIFICATION: 536

C--> 40 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/08/911,423
 34 (B) FILING DATE: 14-AUG-1997
 37 (A) APPLICATION NUMBER: US 60/023,419
 38 (B) FILING DATE: 16-AUG-1996
 41 (A) APPLICATION NUMBER: US 60/027,901
 42 (B) FILING DATE: 07-OCT-1996

C--> 44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Ching, Edwin P.
 46 (B) REGISTRATION NUMBER: 34,090
 47 (C) REFERENCE/DOCKET NUMBER: DX0612K

C--> 49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 650-852-9196
 51 (B) TELEFAX: 650-496-1200

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:
 57 (A) LENGTH: 1073 base pairs
 58 (B) TYPE: nucleic acid
 59 (C) STRANDEDNESS: single

ENTERED

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60 (D) TOPOLOGY: linear
62 (ii) MOLECULE TYPE: cDNA
65 (ix) FEATURE:
66 (A) NAME/KEY: CDS
67 (B) LOCATION: 68..751
70 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
72 CTCGAGATCC ATTGTGCTGG AAAGGGAACCT CCTGAAATCA GCCGACAGAA GACTCAGGAG 60
74 AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT 109
75 Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys
76 1 5 10
78 GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC 157
79 Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly
80 15 20 25 30
82 CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC 205
83 Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser
84 35 40 45
86 CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT 253
87 Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys
88 50 55 60
90 GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG 301
91 Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys
92 65 70 75
94 CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT 349
95 His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile
96 80 85 90
98 GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA 397
99 Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala
100 95 100 105 110
102 GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA 445
103 Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly
104 115 120 125
106 TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC 493
107 Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile
108 130 135 140
110 CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC 541
111 Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe
112 145 150 155
114 CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC 589
115 Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly
116 160 165 170
118 CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC 637
119 Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr
120 175 180 185 190
122 CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC 685
123 Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe
124 195 200 205
126 CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT 733
127 Gln Phe Pro Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His
128 210 215 220

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130 CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC 781
 131 Leu Gly Gly Arg Trp Pro
 132 225
 134 CAGACGCTAC AAGACTTGCC CAGCTATACC CTTGGTGAGA GCAGGGCCA TGCTCTGCAC 841
 136 CCTTCCCTGG GCCTGGCCCT GCTCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG 901
 138 TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT 961
 140 CTTTGGGCC ACCAAGAGCA CCACGTTAG CACAAGATCT TGTACAAGAA TAAATACTTG 1021
 142 TTTAGTAACC TGAAAAAAA AAAAAGG GCGGCCGCGG AGGCCGAATT CC 1073
 145 (2) INFORMATION FOR SEQ ID NO: 2:
 147 (i) SEQUENCE CHARACTERISTICS:
 148 (A) LENGTH: 228 amino acids
 149 (B) TYPE: amino acid
 150 (D) TOPOLOGY: linear
 152 (ii) MOLECULE TYPE: protein
 154 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 156 Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu
 157 1 5 10 15
 159 Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly
 160 20 25 30
 162 Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr
 163 35 40 45
 165 Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr
 166 50 55 60
 168 Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr
 169 65 70 75 80
 171 Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe
 172 85 90 95
 174 Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
 175 100 105 110
 177 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
 178 115 120 125
 180 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
 181 130 135 140
 183 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
 184 145 150 155 160
 186 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
 187 165 170 175
 189 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
 190 180 185 190
 192 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
 193 195 200 205
 195 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
 196 210 215 220
 198 Gly Arg Trp Pro
 199 225
 201 (2) INFORMATION FOR SEQ ID NO: 3:
 203 (i) SEQUENCE CHARACTERISTICS:
 204 (A) LENGTH: 1006 base pairs
 205 (B) TYPE: nucleic acid

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206 (C) STRANDEDNESS: single
 207 (D) TOPOLOGY: linear
 209 (ii) MOLECULE TYPE: cDNA
 212 (ix) FEATURE:
 213 (A) NAME/KEY: CDS
 214 (B) LOCATION: 1..723
 217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 219 ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG 48
 220 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
 221 1 5 10 15
 223 GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC 96
 224 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
 225 20 25 30
 227 GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC 144
 228 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
 229 35 40 45
 231 TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG 192
 232 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
 233 50 55 60
 235 GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC 240
 236 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
 237 65 70 75 80
 239 TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA 288
 240 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
 241 85 90 95
 243 GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT 336
 244 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
 245 100 105 110
 247 ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC 384
 248 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
 249 115 120 125
 251 AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT 432
 252 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
 253 130 135 140
 255 GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA 480
 256 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
 257 145 150 155 160
 259 GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC 528
 260 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
 261 165 170 175
 263 GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG 576
 264 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
 265 180 185 190
 267 AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG 624
 268 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val
 269 195 200 205
 271 CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG 672
 272 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
 273 210 215 220

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275 CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG 720
276 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
277 225 230 235 240
279 GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG 773
280 Val

283 GAGCTCCCA GGCCGCAGGG GCTCTGCCTT CTGCTCTGGG CCGGGCCCTG CTCCCTGGC 833
285 AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTGGCGG 893
287 CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT 953
289 GTCACCTAAA TTCAATTAC C TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA 1006

292 (2) INFORMATION FOR SEQ ID NO: 4:

294 (i) SEQUENCE CHARACTERISTICS:
295 (A) LENGTH: 241 amino acids
296 (B) TYPE: amino acid
297 (D) TOPOLOGY: linear

299 (ii) MOLECULE TYPE: protein

301 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

303 Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu
304 1 5 10 15

306 Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro
307 20 25 30

309 Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg
310 35 40 45

312 Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu
313 50 55 60

315 Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His
316 65 70 75 80

318 Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro
319 85 90 95

321 Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys
322 100 105 110

324 Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys
325 115 120 125

327 Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro
328 130 135 140

330 Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala
331 145 150 155 160

333 Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys
334 165 170 175

336 Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu
337 180 185 190

339 Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Glu Val
340 195 200 205

342 Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu
343 210 215 220

345 Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
346 225 230 235 240

348 Val

351 (2) INFORMATION FOR SEQ ID NO: 5:

353 (i) SEQUENCE CHARACTERISTICS:

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09545998.raw

Output Set: N:\CRF4\07282004\I545998.raw

L:29 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:30 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]
L:35 M:238 W: Alpha Fields not Ordered, Reordered [(C) CLASSIFICATION:] of (1) (vi)
L:36 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:40 M:220 C: Keyword misspelled or invalid format, [(vii) PRIOR APPLICATION DATA:]
L:44 M:220 C: Keyword misspelled or invalid format, [(viii) ATTORNEY/AGENT INFORMATION:]
L:49 M:220 C: Keyword misspelled or invalid format, [(ix) TELECOMMUNICATION INFORMATION:]